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Title:
Perfect score:
                                                                                                                                                                            OM protein - protein search, using sw model
    Sequence:
                                                                                                                                     Run on:
                                                                                  March 1, 2001, 16:17:05; Search time 17.21 Seconds (without alignments) 112.588 Million cell updates/sec
US-09-331-631A-22_COPY_25_84
350
1 EDDNHHHHGGHKSGQCVRRC.....EKRQERSRHEADDRSGEGSS 60
                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

31 32 33	29 30	27 28	26	25 25	2 3	22	21	20	10	17	16	15	1.4	13	12	11	10	9	œ ·	7	ט ת	4.1	ω	N	- 1	No.	Result
62 62	62.5 62.5	62.5	63	5 G	5 6	63	63	63.5	, , ,	0 0	65.5	65.5	65.5	65.5	65.5	66	on.	67.5		500	69. 60. 60.	` 7	78	•	₽-	Score	
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Query Match

98.9%; Score 346; DB 1; Length 573;

ALIGNMENTS

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SFR4_HUMAN
ID SFR4_H
AC QOB170
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Matches 17
                                                              SFR4_HUMAN
Q08170;
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30-MAY-2000
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SEQUENCE
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15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
Gossypium hirsutum (Upland cotton).
Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chian C.A., Borroto K., Kamalay J.A., Dure L. III;
"Developmental biochemistry of cottonseed embryogenesis
germination. XIX. Sequences and genomic organization of
globulin (vicilin) genes of cottonseed.";
Plant Mol. Biol. 9:533-546(1987).
-!- FUNCTION: SEED STORAGE PROTEIN.
                                                     SPLICING FACTOR,
                                                                                                                                                                                                                                                                      SIGNAL
              Eukaryota;
                      Homo sapiens
                                   SFRS4 OR SRP75
                                                                                                                                                                                                                                                                         Seed storage protein; Signal
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                   EMBL; M19378; AAA33069.1;
                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                        modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnoliophyta; eudicotyledons; core Malvales; Malvaceae; Gossypium.
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                                                                                                                                                                      QCVRRC----EDRPWHQRPRCLEQCREEERE-----KRQERSRHEADDRSGEG
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                                                                                                                                                                                                 17; Conservative
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59; Conservative
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              Metazoa;
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                                                    (Rel. 31, Last sequence up
(Rel. 39, Last annotation
CTOR, ARGININE/SERINE-RICH
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                       (Human
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            Chordata;
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Pred. No. 0.28
15; Mismatches
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1; Mismatches
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              Craniata;
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              Euteleostomi;
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Best Local
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
MEDLINE=91244309; PubMed=2037293;
Hofmann S.L., Topham M., Hsieh C.L.,
Topham And genomic cloning of HRC, a
                                                                                                                                                                                                                                                                                                                       DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                      SRCH_HUMAN STA
P23327;
01-NOV-1991 (Rel.
                                                                                                                                                                                         HUMAN
                                                                                                                            SARCOPLASMIC
                                                                                                                                    01-NOV-1991
15-JUL-1999
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MIM; 601940;
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                                                                         Mammalla;
                                                                                    Eukaryota;
                                                                                                        HRC OR HCP
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                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DURING PRE-MRNA SPLICING. SUBCELLULAR LOCATION: NUCLEAR PTM: EXTENSIVELY PHOSPHORYLAT
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SIMILARITY:
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European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                        L14076; AAA36649.1;
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19; Conserv
                                                                        ; Metazoa;
Eutheria;
                                                               s (Human).
Metazoa; Chordata; C
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35
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            human
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SEQUENCE OF 35-45; 84-89; 126-137; 140-154 AND MEDLINE=92249775; Pubmed=1577277; Zahler A.M., Lane W.S., Stolk J.A., Roth M.B.; "SR proteins: a conserved family of pre-mRNA spl Genes Dev. 6:837-847(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"Human SR proteins and isolation of a cDNA
Mol. Cell. Biol. 13:4023-4028(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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BELONGS TO THE SR FAMILY OF SPLICING FACTORS
                                                                                                                                                                                                                                    20, Created)
20, Last sequence update)
38, Last annotation update)
38, Last annotation update)
DULUM HISTIDINE-RICH CALCIUM-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB Pred. No. 0.51 7; Mismatches
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                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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ງ.51;
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sarcoplasmic
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01-FEB-1994
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 STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson
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DOMAIN
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P34623;
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                                                                                          Nicholas J., Cameron K.R., Coleman H., Newman C., Honess "Analysis of nucleotide sequence of the rightmost 43 kbp herpesvirus saimiri (HVS) L-DNA: general conservation of organization between HVS and Epstein-Barr virus.";
Virology 188:296-310(1992).
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IE68_HSVSA
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Hypothetical
SEQUENCE 24
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MEDLINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Camero Albrecht J.-C., Coleman
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                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92230228; PubMed=1314457;
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Viruses; dsDNA viruses, no RNA s
Gammaherpesvirinae; Rhadinovirus
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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             European Bioinformatics Institute.
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                          structure of the herpesvirus . 66:5047-5058(1992).
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                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                   PIR; A30838; FWCNAB. HSSP; P50477; 1CAX.
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
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-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
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SIMILARITY:
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PROSITE; PS00303; S100_CABP;
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TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUE:
THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA,
THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABI
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION
THE EPIDERMIS.
                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinf
European Bioinformatics Institute
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PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES
PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES
PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 2010 ARGININES
PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 2010 ARGININES
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                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                               S28589; S28589.
; P02633; 1BOC.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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30, Last sequence up
40, Last annotation
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S-100 LIKE.
SITE I (LOW AFFINITY) (POTENTIAL).
SITE II (HIGH AFFINITY) (POTENTIAL)
MW; AE17D2A159F12B7F CRC64;
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                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
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Caenorhabditis elegans.
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 8 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
01-NOV-1997 (Rel. 35,
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                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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                                             EDDNHHHHGGHKSGQCVRRCEDRPWH-QRPRCLEQCREEEREKRQERS-----RHEAD 52
EEKKKDKHGREEKRDRRRRSNDRHGRDRRSRSRSQSRDRNR-RRDDRSGRDGRVGRNERD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                        Similarity
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PS50072; CSA_PPIASE_2; 1.
se; Rotamase; Multigene family.
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Pred. No. 5.4;
7; Mismatches
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RA KINDELS, JUNG H.H., PARK S.H., CHIN H.;

RA KINDELS, JUNG H.H., PARK S.H., CHIN H.;

RA KINDELS, JUNG H.H., PARK S.H., CHIN H.;

RESUMMITTED (FEB-1997) to the EMBL/GenBank/DDBJ databases.

CC 11- FUNCTION: VOLTAGE-SENSITYVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED COLOR OF CALCIUM HONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED COLOR OF CALCIUM HONS ON REUROTRANSMITTER RELEASE, GENE EXPRESSION, COLOR OF THE "HIGH VOLTAGE ACTIVATED" (HVA) GROUP AND ALPHA-1B CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS COLOR TO THE "HIGH VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CAGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHECTED MIGRATION OF IMMATURE NEURONS.

CC DIHYDROPPREDIBLES CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN CALCIUM CHANNELS ARE MULTISUBUNIT COLOR DIRECTED MIGRATION OF IMMATURE NEURONS.

CC DISCONDINCT SUBURITY. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. SUBUNITS SUBUNIT SUBUNITS SUBUNIT SUBUNITS. THE AUXILIARY SUBUNITS TO AND ALPHA-2/DELTA AND ALPHA-2/DELTA CC LINKED BY A DISCULTIVE BRAUGHT THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SUBCELLULAR FORDUCTS: 2 ISOFORMS; ALPHA-1B-1 (SHOWN HERE) AND CLIMA-1B-2, HARE PRODUCED BY ALTERNATIVE SPLICIUM.

CC -1- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CHANNEL ACTIVITY.

CC -1- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CHANNEL ACTIVITY.

CC -1- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CHANNEL ACCHOR OR ACTION ALPHA-1B-1 AND ALPHA-1B-1 (SHOWN HERE) AND ONE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC FORDABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- THE FOUR THE FOUR THE FOUR THE SENSOR AND ARE CHARACTERIZED BY A SENSOR AND ARE CHARACTERIZED BY A 
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-0CT-2000 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
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TISSUE=LUNG FIBROBLAST;
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SIMILARITY: BELONGS
FAMILY.
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                                                                                                                                                            EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$1 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$2 OF REPEAT IV (POTENTIAL).

$3 OF REPEAT IV (POTENTIAL).

$3 OF REPEAT IV (POTENTIAL).

$4 OF REPEAT IV (POTENTIAL).

$4 OF REPEAT IV (POTENTIAL).
                     BINDING TO THE B SIMILARITY).
ATP (POTENTIAL).
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S1 OF REPEAT II (POTENTIAL)
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S2 OF REPEAT II (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
S3 OF REPEAT II (POTENTIAL)
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CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                         EXTRACELLULAR (POTENTIAL)
S6 OF REPEAT IV (POTENTIA
                                                                                                                                    CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT III (POTENTIAL).
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S2 OF REPEAT III (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
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S5 OF REPEAT
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S1 OF REPEAT III (POTENTIAL).
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S5 OF REPEAT II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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S4 OF REPEAT II (POTENTIAL).
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S6 OF REPEAT I (POTENTIAL).
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S5 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL)
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S1 OF REPEAT I (POTENTIAL)
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OF REPEAT III (POTENTIAL).
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GSGSVNGSPLLSTSGASTPGRGGRQLPOTPLTPRPSTTYK
TANSSP1HFAGAQTSLDAFSPGRLSRGLSEHAALLQRDPLS
QPLAPGSRIGSDPYLGQRLDSEASVHALLEDTLTFEERAVAT
NSGRSSRTSYVSSLTSOSHPLRRVPNGYHCTLGLSSGGRAR
HSYHHPDQDHWC -> AGSAVGFPWTTPCCRETPSASPWPL
ALELALTLTWGSVWTVRPLSTPCLRTRSLSRRLWPPTRAAP
PGLPTCPP (IN ISONOMM ALPHA-1B-2).
                                                                                 Score 66; DB
Pred. No. 32;
7; Mismatches
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PHOSPHORYLATION (BY CAPE
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CALCIUM ION SELECTIVITY (BY SIMILARITY).
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-!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTTVATED" (HVA) GROUP AND ARE BLOCKED IIIA (OMEGA-GA-IIIA). THEY ARE HOMEYER INSENSITIVE TO DIFFUNDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGATOXIN GALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.
-!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS Q05152; 15-JUL-1999 (Rel.: 15-JUL-1999 (Rel.: 15-JUL-1999 (Rel.: 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHAN Mikoshiba K., Mori Y., Beam K.G.;
"Primary structure and functional expression of the osensitive N-type calcium channel from rabbit brain.";
Neuron 10:585-598(1993). Friedrich T., Iwabe N., Miyata 7 MEDLINE=93236885; PubMed=8386525; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; TISSUE=BRAIN; SEQUENCE FROM N.A. CACNAIB OR CACNLIAS OR CACHS CCAB_RABIT STANDARD; Miyata T., Furuichi T., R.T., 2339 Kim Ş M. -S., Furutama (BRAIN CALCIUM CHANNEL Niidome omega-conotoxin-□] ; ; Nakai ت . ر

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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

"IS SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"IT TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN. HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.

"ID DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THERD POSITION.

"IT PIM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
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S; PR00167; CACHANNEL.
channel; Transmembrane; I
um_channel; Glycoprotein;
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                                                                EXTRACELLULAR (POTENTIAL).

$4 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT II (POTENTIAL).

$5 OF REPEAT II (POTENTIAL).

$6 OF REPEAT II (POTENTIAL).

$6 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$1 OF REPEAT III (POTENTIAL).

$2 OF REPEAT III (POTENTIAL).

$2 OF REPEAT III (POTENTIAL).

$3 OF REPEAT III (POTENTIAL).

$3 OF REPEAT III (POTENTIAL).
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$4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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$1 OF REPEAT II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$2 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
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                                        EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT III (POTENTIAL)
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S3 OF REPEAT II (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
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S1 OF REPEAT I (POTENTIAL).
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15-JUL-1998
PROTEIN U79.
                                                                                                                       U79 OR CB/R.
U79 OR CB/R.
Herpes simplex virus (type 6 / strain Z29).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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TRANSMEM
"Restriction endonuclease mapping and molecular cloning of the hur herpesvirus 6 variant B strain 229 genome."; Arch. Virol. 141:367-379(1996).
-i- FUNCTION: POSSIBLE REPLICATION PROTEIN.
-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND HSV-7 U79 AND HCMV UL112 (P34).
                                                                 Lindquester G.J., Inoue N., Allen R.D., Constamey F.R., Dambaugh T.R., O'Brian J.J., Frenkel N., Pellett P.E.;
                                                                                                                                                                                                                                                                                        2100
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                                                                                                                                                                                                                                                                                                                                                      4 NHHHHGGHKSGQCVRRCEDRPWHQRPRCLEQ-----
                                                                                                                                                                                                                                                                                                                                  HHHHH-----RCHRR-RDR----KQRSLEKGPSLSADTDGAPDSTVGPGLPTGEGPPGC 2099
                                                                                                                                                                                                                                                                                       R-RERERRQERGRSQERRQPSSSSS
                                                                                                                                                                                                                                                                                                            REEEREKRQERSRHEADDRSGEGSS
                                                                                                                                                                                                                                                                                                                                                                            Similarity 28.:
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 1740
256
1566
1678
2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1370
                                                                                                                                                                                  (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 36, Last annotation updat
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1422
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1496
1151
1153
1153
1539
1558
1567
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                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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1751
256
1566
1678
A; 261178
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                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).

PHOSPHORVLATION (BY CAPK) (POTENTIAL PHOSPHORVLARITY).

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB Pred. No. 32; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S6 OF REPEAT
CYTOPLASMIC
S1 OF REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT IV (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY). CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY.
BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                        2123
                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT III (POTENTIAL)
                                                                                                                                                                                                                                 345
                                                                                       Castelli J
                                                                                                                                                                                                                                  Ą
                                                                              Danovich
                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA SUBUNIT (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY CAPK) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               Length 2339
                                                                            7 R.M.
                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                       ----c
                                                        human
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RESULT 13
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Best Local S
Matches 14
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15-JUL-1999
INTERSECTIN
                                               DOMAIN
                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        Chen H., Antonarakis S.E.; "The SH3DIA gene maps to human chromosome Cytogenet. Cell Genet. 78:213-215(1997).
                                                                                                   PFAM; PF00018;
                                                                                                                           MIM; 602442;
                                                                                                                                       HSSP; P29354;
                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITSN_HUMAN
Q15811;
 SEQUENCE
              DOMAIN
                          DOMAIN
                                       DOMAIN
                                                                          PROSITE;
                                                                                     PRINTS; PR00452; SH3DOMAIN
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                               containing proteins
                                                                                                                                                                                                                                                                                                                                                                                           Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., "Cloning of ligand targets: systematic isolation of SH3 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L14772; AAB06363.1; -.
SEQUENCE 345 AA; 39579 MW; E2CC942C85D4975C CRC64;
                                                                                                              INTERPRO; IPR001452; -
                                                                                                                                                                                                                                                                                                                                MEDLINE=98127038; PubMed=9465890
                                                                                                                                                                                                                                                                                                                                             GENE MAPPING
                                                                                                                                                                                                                                                                                                                                                                    Nat. Biotechnol. 14:741-744(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98294438; PubMed=9630982;
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITSN OR SH3D1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                domain;
                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 4 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDEHRKRSGKQKEK--RKVED-----IDKKKEDEKRKQEEKKRNDEDKR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDNHHHHGGHKSGQCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                            PS50002;
                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
 520
                                                             Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 38, Last annotation update)
(SH3 DOMAIN-CONTAINING PROTEIN SH3P17).
                                                                                                                                        1GFD.
                                                                                                                                                    AAC50592.1;
 AA,
                                                                                                   SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                         SH3;
              177
342
438
514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
 57976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%;
26.4%;
 MW;
           SH3.
SH3.
SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
614043F1DB098C60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Length 345;
                                                                                                                                                                                                                                         and the
                                                                                                                                                                                                      bу
                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                            , Kay B.K.;
domain-
                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                          a collaboration
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                                                                                                                                                                                                      commercia:
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH, THE ISOFORM ALPHA-1E
GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
AGA-IVA). CALCIUM CHANNELS CONTANING ALPHA-1E SUBUNIT COULD BE
INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
INPORTANT FOR INFORMATION PROCESSING.
IN A 1:1:1:1 RAPTO. THE CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RAPTO. THE CHANNEL ACTIVITY IS DIFECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

THE SUBUNIT IS SUFFICIENT TO SENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

THE SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAE_RAT
Q07652;
                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE-93262464; PubMed-8388125;
Soong T.W., Stea A., Hodson C.D., Du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activated calcium channel f
Science 260:1133-1136(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACNAlE OK CACHAEL (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRAIN CALCIUM CHANNEL II) (BII). CACNAlE OR CACNLIA6 OR CACH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snutch T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (RBE-II) (RBE2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure and functional expression of a member of the low voltage-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 RRAQERDKQWLEHVQQEDEHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLG
                                                                                                                                                                                                                                SIMILARITY: FAMILY.
                                                                                                                                                                                                                                               HYDROPHOBIC TRANSMEMBRANE SEGMENTS ($1, $2, $3, $5, $6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT ($4). $4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED ANINO ACIDS AT EVERY THIRD POSITION SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
                                                                                                                                                                                                                                                                                                                                                          DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
                                                                                                                                                                                                                                                                                                                                                                                INSULINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRCE--DRPW-----HQRPRCL---EQCREEEREKR---QERSRHEADDRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%;
33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.";
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Pred. No. 9.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dubel S.J., Vincent S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2222
                                                                                                                                       There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 520;
                                                                                                                                           restrictions on
                                                                                                                                                                   EMBL
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                                                                                                                                                                   collaboration -
L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
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EMBL; L15453;

AAA40855.1;

INTERPRO;

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TRANSMEM
DOMAIN
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REPEAT 27 305 I.
REPEAT 413 657 II.
REPEAT 1092 1378 III.
REPEAT 1415 1678 IV.
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Calcium channel; Glycoprotein; Repeat; Multigene family;
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S1 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

S4 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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S3 OF REPEAT II (POTENTIAL).
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S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT II (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
(BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
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POLY-VAL.
POLY-ARG.
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POLY-ARG.
POLY-ARG.
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S3 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
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SIMILARITY).
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S5 OF REPEAT IV (POTENTIAL).
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S2 OF REPEAT II (POTENTIAL).
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S6 OF REPEAT IV (POTENTIA
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S1 OF REPEAT II (POTENTIAL).
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S2 OF REPEAT I (POTENTIAL)
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S1 OF REPEAT
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                                                      RL J. Biol. Chem. 269:2347-22357(1994).

RL J. Biol. Chem. 269:2347-22357(1994).

CC -i- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC LIN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E CC GIVES RISE TO R-TYPE CALCIUM CHRRENTS. R-TYPE CALCIUM CHANNELS

CC GIVES RISE TO R-TYPE CALCIUM CHRRENTS. R-TYPE CALCIUM CHANNELS

CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIA (OMEGA-AGA-IIIA).

CC GIVES RISE TO R-TYPE CALCIUM CHANNELS (DHP), OMEGA-AGA-IIIA).

CC CONTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IIIA).

CC CONTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTANING ALPHA-1E SUBUNIT COULD BE CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS INVOLVED IN THE MODULATION PROCESSING.

CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT SC INFORMATION OF FIRING PATTERNS OF NEURONS WHICH IS COMPLEXES, CONSISTING OF ALPHA-1, ACTIVITY IS DIRECTED BY THE PORE-CC IN A 1:::1:1 RATIO. THE CHANNEL ACTIVITY SETA AND ALPHA-2/DELTA SUBUNITS SUBUNITS SUBUNITS IS SUBUNITS. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CC LINKED BY A DISULETDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -I- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -INSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES, RETINA, SPLEEN, AND ALPHA-1 SUBUNITS SETA AND ALPHA-2/DELTA CCC -INSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES, RETINA, SPLEEN, AND ADAPTATE COLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAE_MOUSE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAE_MOUSE STANDARD; PRT; 2272 AA. 061290; 061290; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) VOLTAGE-EEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM CHANNEL, TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM CHANNEL II) (BII).
CHANNEL II) (BII).
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SEQUENCE
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MOD_RES
CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams M.E., Marubio L.M., Deal C.R., Hans Nehilipson L.H., Miller R.J., Johnson E.C., Har "Structure and functional characterization of calcium channel subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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AND PANCREATIC ISLET CELLS.

AND PANCREATIC THE FOUR INTERNAL REPEATS CO

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CO

TO THE FOUR INTERNAL REPEATS (S1, S2,
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l Similarity 32.4%;
23; Conservative
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(hordata;
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N-DF6452A2175CEB19 CRC
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(BY SIMILARITY).
BY SIMILARITY
PHOSPHORYLATION (BY CAPK)
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N-LINKED (GLCNAC. . .) (P
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Pred. No. 34;
9; Mismatches
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Harpold M.M., Ellis
of neuronal alpha 1
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                       CONTAINS
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPRO00636; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITIVELY CHARGED TRANSMEMBRANE SEGMENT ($4). $4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F00520; ion_trans; 4.
PR00167; CACHANNEL.
hannel; Transmembrane;
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CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S3 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT II (POTENTIAL).

EXTRACELULAR (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

EXTRACELULAR (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).
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S4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).

54 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

55 OF REPEAT IV (POTENTIAL).
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S4 OF REPEAT III (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III (POTENTIAL)
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S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
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; Repeat; Multigene family;
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THE PRESENTATION OF THE PR

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Best Local S
Matches 23
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BY SIMILARITY.
PHOSENGRYLATION (BY CAPK) (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                          Score 65.5; D
Pred. No. 35;
9; Mismatches
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POLY-ARG.
BINDING T
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POLY-GLU.
POLY-LYS.
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CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
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CALCIUM ION SELECTIVITY AND PERMEABILITY
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S6 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                       POLY-ARG.
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                                                                                            DB
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                                                                                           Length 2272;
                                                                          Indels
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4.

Search completed: March 1, 2001, 16:20:32 Job time: 207 sec